



1/12

SEQUENCE LISTING

<110> Sahni, Girish
Kumar, Rajesh
Roy, Chaiti
Rajagopal, Kammara
Nihalani, Deepak
Sundaram, Vasudha
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
PREPARATION OF SAID PROTEINS

<130> 07064/009001

<140> US 09/471,349

<141> 1999-12-23

<150> IN 3825/DEL/98

<151> 1998-12-24

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1245

<212> DNA

<213> Streptococcus equisimilis

<220>

<221> CDS

<222> (1)...(1242)

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caa tta gtt gtt agc gtt gct ggt act gtt gag ggg acg aat caa gac 96
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp
20 25 30

att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat 144
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His
35 40 45

gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct 192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala
50 55 60

act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta 240
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu
65 70 75 80

aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac 288
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp
85 90 95

tac	ttt	gag	gtc	att	gat	ttt	gca	agc	gat	gca	acc	att	act	gat	cga	336
Tyr	Phe	Glu	Val	Ile	Asp	Phe	Ala	Ser	Asp	Ala	Thr	Ile	Thr	Asp	Arg	
		100						105					110			
aac	ggc	aag	gtc	tac	ttt	gct	gac	aaa	gat	ggg	tcg	gta	acc	ttg	ccg	384
Asn	Gly	Lys	Val	Tyr	Phe	Ala	Asp	Lys	Asp	Gly	Ser	Val	Thr	Leu	Pro	
		115					120					125				
acc	caa	cct	gtc	caa	gaa	ttt	ttg	cta	agc	gga	cat	gtg	cgc	gtt	aga	432
Thr	Gln	Pro	Val	Gln	Glu	Phe	Leu	Leu	Ser	Gly	His	Val	Arg	Val	Arg	
	130					135					140					
cca	tat	aaa	gaa	aaa	cca	ata	caa	aac	caa	gcg	aaa	tct	gtt	gat	gtg	480
Pro	Tyr	Lys	Glu	Lys	Pro	Ile	Gln	Asn	Gln	Lys	Ser	Val	Asp	Val		
145					150				155					160		
gaa	tat	act	gta	cag	ttt	act	ccc	tta	aac	cct	gat	gac	gat	ttc	aga	528
Glu	Tyr	Thr	Val	Gln	Phe	Thr	Pro	Leu	Asn	Pro	Asp	Asp	Asp	Phe	Arg	
			165					170						175		
cca	ggg	ctc	aaa	gat	act	aag	cta	ttg	aaa	aca	cta	gct	atc	ggg	gac	576
Pro	Gly	Leu	Lys	Asp	Thr	Lys	Leu	Leu	Lys	Thr	Leu	Ala	Ile	Gly	Asp	
		180					185						190			
acc	atc	aca	tct	caa	gaa	tta	cta	gct	caa	gca	caa	agc	att	tta	aac	624
Thr	Ile	Thr	Ser	Gln	Glu	Leu	Leu	Ala	Gln	Ala	Gln	Ser	Ile	Leu	Asn	
		195					200					205				
aaa	aac	cac	cca	ggc	tat	acg	att	tat	gaa	cgt	gac	tcc	tca	atc	gtc	672
Lys	Asn	His	Pro	Gly	Tyr	Thr	Ile	Tyr	Glu	Arg	Asp	Ser	Ser	Ile	Val	
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Thr	His	Asp	Asn	Asp	Ile	Phe	Arg	Thr	Ile	Leu	Pro	Met	Asp	Gln	Glu	
225					230					235				240		
ttt	act	tac	cgt	gtt	aaa	aat	cgg	gaa	caa	gct	tat	agg	atc	aat	aaa	768
Phe	Thr	Tyr	Arg	Val	Lys	Asn	Arg	Glu	Gln	Ala	Tyr	Arg	Ile	Asn	Lys	
			245					250						255		
aaa	tct	ggg	ctg	aat	gaa	gaa	ata	aac	aac	act	gac	ctg	atc	tct	gag	816
Lys	Ser	Gly	Leu	Asn	Glu	Glu	Ile	Asn	Asn	Thr	Asp	Leu	Ile	Ser	Glu	
		260					265						270			
aaa	tat	tac	gtc	ctt	aaa	aaa	ggg	gaa	aag	ccg	tat	gat	ccc	ttt	gat	864
Lys	Tyr	Tyr	Val	Leu	Lys	Lys	Gly	Glu	Lys	Pro	Tyr	Asp	Pro	Phe	Asp	
		275					280					285				
cgc	agt	cac	ttg	aaa	ctg	ttc	acc	atc	aaa	tac	gtt	gat	gtc	gat	acc	912
Arg	Ser	His	Leu	Lys	Leu	Phe	Thr	Ile	Lys	Tyr	Val	Asp	Val	Asp	Thr	
	290					295					300					
aac	gaa	ttg	cta	aaa	agt	gag	cag	ctc	tta	aca	gct	agc	gaa	cgt	aac	960
Asn	Glu	Leu	Leu	Lys	Ser	Glu	Gln	Leu	Leu	Thr	Ala	Ser	Glu	Arg	Asn	
305					310					315					320	
tta	gac	ttc	aga	gat	tta	tac	gat	cct	cgt	gat	aag	gct	aaa	cta	ctc	1008
Leu	Asp	Phe	Arg	Asp	Leu	Tyr	Asp	Pro	Arg	Asp	Lys	Ala	Lys	Leu	Leu	
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tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga	1056
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly	
340 345 350	
aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat	1104
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr	
355 360 365	
atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat	1152
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr	
370 375 380	
gat aaa gat cgt tat acc gaa gaa gaa cga gaa gtt tac agc tac ctg	1200
Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu	
385 390 395 400	
cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa	1242
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys	
405 410	
taa	1245

<210> 2

<211> 414

<212> PRT

<213> Streptococcus equisimilis

<400> 2

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Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His	
35 40 45	
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala	
50 55 60	
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu	
65 70 75 80	
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp	
85 90 95	
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg	
100 105 110	
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro	
115 120 125	
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg	
130 135 140	
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val	
145 150 155 160	
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg	
165 170 175	
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp	
180 185 190	
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn	
195 200 205	
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val	
210 215 220	
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu	
225 230 235 240	
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys	
245 250 255	
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu	
260 265 270	

Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp
 275 280 285
 Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr
 290 295 300
 Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn
 305 310 315 320
 Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu
 325 330 335
 Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly
 340 345 350
 Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr
 355 360 365
 Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr
 370 375 380
 Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu
 385 390 395 400
 Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys
 405 410

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(777)

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 agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa 96
 Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 20 25 30
 cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat 144
 Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
 35 40 45
 gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag 192
 Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
 50 55 60
 act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act 240
 Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
 65 70 75 80
 tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg 288
 Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
 85 90 95
 gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa 336
 Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
 100 105 110
 ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag 384
 Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
 115 120 125

act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga	432
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly	
130 135 140	
gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct	480
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala	
145 150 155 160	
ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc	528
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly	
165 170 175	
tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc	576
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile	
180 185 190	
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc	624
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser	
195 200 205	
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg	672
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu	
210 215 220	
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag	720
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Glu Trp Lys Cys Glu	
225 230 235 240	
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc	768
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr	
245 250 255	
gat gtt cgt	777
Asp Val Arg	

<210> 4
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 4
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 20 25 30
 Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
 35 40 45
 Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
 50 55 60
 Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
 65 70 75 80
 Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
 85 90 95
 Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
 100 105 110
 Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
 115 120 125
 Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
 130 135 140

Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
 145 150 155 160
 Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
 165 170 175
 Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
 180 185 190
 Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
 195 200 205
 Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
 210 215 220
 Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
 225 230 235 240
 Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
 245 250 255
 Asp Val Arg

<210> 5
 <211> 1377
 <212> DNA
 <213> Streptococcus equisimilis

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 agatatacca tgattgctgg acctgagtgg ctgctagacc gtccatctgt caacaacagc 180
 caattgggtg ttagcggttg tggtagctgt gaggggacga atcaagacat tagtcttaaa 240
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 ccaggtctca aagatactaa gctattgaaa acactagcta tcggtgacac catcacatct 720
 caagaattac tagctcaagc acaaagcatt ttaaacaaaa accaccagag ctatacgatt 780
 tatgaacgtg actcctcaat cgtcactcat gacaatgaca ttttcctgac gattttacca 840
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 aaatctgggtc tgaatgaaga aataaacaac actgacctga tctctgagaa atattacgtc 960
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 atcaaatacg ttgatgtcga taccaacgaa ttgctaaaaa gtgagcagct cttaacagct 1080
 agcgaacgta acttagactt cagagattta tacgatcctc gtgataaggc taaactactc 1140
 tacaacaatc tcgatgcttt tggattatag gactatacct taactggaaa agtagaggat 1200
 aatcacgatg acaccaaccg tatcataacc gtttatatgg gcaagcgacc cgaaggagag 1260
 aatgctagct atcatttagc ctatgataaa gatcggtata ccgaagaaga acgagaagtt 1320
 tacagctacc tgcgttatac agggacacct atacctgata accctaacga caaataa 1377

<210> 6
 <211> 1327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

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 aaataacagc caattgggtg ttagcggttg tggtagctgt gaggggacga atcaagacat 180
 tagtcttaaa ttttttgaaa tcgatctaac atcacgacct gctcatggag gaaagacaga 240
 gcaaggctta agtccaaaat caaaaccatt tgctactgat agtggcgcg tgtcacataa 300
 acttgagaaa gctgacttac taaaggctat tcaagaacaa ttgatcgcta acgtccacag 360

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cggcaaggtc	tactttgctg	acaaagatgg	ttcggtaacc	ttgccgaccc	aacctgtcca	480
agaatttttg	ctaagcggac	atgtgcgctg	tagaccatat	aaagaaaaac	caatacaaaa	540
ccaagcgaaa	tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	accctgatga	600
cgatttcaga	ccaggtctca	aagatactaa	gctattgaaa	acactagcta	tcggtgacac	660
catcacatct	caagaattac	tagctcaagc	acaaagcatt	ttaaacaaaa	accaccagg	720
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cttaacagct	agcgaacgta	acttagactt	cagagattta	tacgatcctc	gtgataaggc	1080
taaactactc	tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	taactggaaa	1140
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cgaaggagag	aatgctagct	atcatttagc	ctatgataaa	gatcgttata	ccgaagaaga	1260
acgagaagtt	tacagctacc	tcggttatac	agggacacct	atacctgata	accctaacga	1320
caaataa						1327

<210> 7

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<221> CDS

<222> (2)...(52)

<400> 7

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ccc

Pro

52

<210> 8

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated protein

<400> 8

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Pro

<210> 9

<211> 1541

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 9

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atcaagacat	tagtcttaaa	ttttttgaaa	tcgatctaac	atcacgacct	gctcatggag	180
gaaagacaga	gcaaggctta	agtccaaaat	caaaaccatt	tgctactgat	agtggcgcgga	240
tgtcacataa	acttgagaaa	gctgacttac	taaaggctat	tcaagaacaa	ttgatcgcta	300
acgtccacag	taacgacgac	tactttgagg	tcattgattt	tgcaagcgat	gcaaccatta	360
ctgatcgaaa	cggcaaggtc	tactttgctg	acaaagatgg	ttcggttaacc	ttgccgaccc	420
aacctgtcca	agaatttttg	ctaagcggac	atgtgcgcgt	tagaccatat	aaagaaaaac	480
caatacaaaa	ccaagcgaaa	tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	540
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tcggtgacac	catcacatct	caagaattac	tagctcaagc	acaaagcatt	ttaaacaaaa	660
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ttttccgtac	gattttacca	atggatcaag	agtttactta	ccgtgttaaa	aatcgggaac	780
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gtgataaggc	taaactactc	tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	1080
taactggaaa	agttagggat	aatcacgatg	acaccaaccg	tatcataacc	gtttatatgg	1140
gcaagcgacc	cgaaggagag	aatgctagct	accatttagc	tggtgggtggc	caggcgcaac	1200
agattgtacc	catagctgag	aagtgttttg	atcatgctgc	tggtgacttc	tatgtggtcg	1260
gagaaacgtg	ggagaagccc	taccaaggct	ggatgatggt	agattgtact	tgcttgggag	1320
aaggcagcgg	acgcatcact	tgcaactcta	gaaatagatg	caacgatcag	gacacaagga	1380
catcctatag	aattggagac	acctggagca	agaaggataa	tcgaggaaaac	ctgctccagt	1440
gcactctgac	aggcaacggc	cgaggagagt	ggaagtgtga	gaggcacacc	tctgtgcaga	1500
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<210> 10

<211> 1661

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 10

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agaccacaac	ggtttccctc	tagaaataat	tttgtttaac	tttaagaagg	agatatacca	180
tgattgctgg	acctgagtgg	ctgctagacc	gtccatctgt	caacaacagc	caattggttg	240
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<211> 1782

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 11

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<211> 2096

<212> DNA

<213> Artificial Sequence

<220>

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<210> 14

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

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<212> DNA

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<220>
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<400> 24
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